

<110> NATIONAL INSTITUTE OF ADVANCED INDUSTRIAL SCIENCE AND TECHNOLOGY  
AMERSHAM BIOSCIENCES KK

<120> Novel acetylgalactosamine transferases and nucleic acids encoding  
the same

<130> 159-86

<140> 10/524,505

<141> 2005-02-14

<150> PCT/JP03/10309

<151> 2003-08-13

<150> JP2002-236292

<151> 2002-08-14

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<212> PRT

<213> Homo sapiens

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Gly Gly Ala Gly Arg Leu Pro Leu Asn Phe Thr His Gln Thr Pro Pro  
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Phe Val Gly Lys Thr Gly Ser Glu Trp Thr Ala Pro Gly Glu Phe Thr						
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<212> DNA

<213> Homo sapiens

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Trp Cys Gly Gly Ala Val Gly His Leu Arg Arg Asn Leu His Phe Pro	
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 Ala Lys Ala Leu Ala Ser Arg Asn Ile Pro Ala Val Asp Pro His Leu  
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Pro	Trp	Leu	Ser	Glu	Phe	Arg	Gly	Arg	Ala	Asn	Leu	His	Val	Phe	Glu	115	120	125
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Pro	Leu	Tyr	Pro	His	Ile	Arg	Thr	Thr	Leu	Arg	Lys	Leu	Ala	Val	Ser	145	150	155
Pro	Lys	Trp	Thr	Asn	Tyr	Gly	Leu	Arg	Ile	Phe	Gly	Tyr	Leu	His	Pro	165	170	175
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Glu	Phe	Trp	Leu	Ser	Leu	Asp	Asp	Gln	Val	Ser	Gly	Leu	Gln	Leu	Leu	195	200	205
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Gly	Lys	Phe	Arg	Ser	Gln	Ile	Ser	Lys	Pro	Val	Ser	Leu	Ser	Ala	Ser	225	230	235
His	Arg	Tyr	Tyr	Phe	Glu	Val	Leu	His	Lys	Gln	Asn	Glu	Glu	Gly	Thr	245	250	255
Asp	His	Val	Glu	Val	Ala	Trp	Arg	Arg	Asn	Asp	Pro	Gly	Ala	Lys	Phe	260	265	270
Thr	Ile	Ile	Asp	Ser	Leu	Ser	Leu	Ser	Leu	Phe	Thr	Asn	Glu	Thr	Phe	275	280	285
Leu	Gln	Met	Asp	Glu	Val	Gly	His	Ile	Pro	Gln	Thr	Ala	Ala	Ser	His	290	295	300
Val	Asp	Ser	Ser	Asn	Ala	Leu	Pro	Arg	Asp	Glu	Gln	Pro	Pro	Ala	Asp	305	310	315
Met	Leu	Arg	Pro	Asp	Pro	Arg	Asp	Thr	Leu	Tyr	Arg	Val	Pro	Leu	Ile	325	330	335
Pro	Lys	Ser	His	Leu	Arg	His	Val	Leu	Pro	Asp	Cys	Pro	Tyr	Lys	Pro	340	345	350
Ser	Tyr	Leu	Val	Asp	Gly	Leu	Pro	Leu	Gln	Arg	Tyr	Gln	Gly	Leu	Arg	355	360	365
Phe	Val	His	Leu	Ser	Phe	Val	Tyr	Pro	Asn	Asp	Tyr	Thr	Arg	Leu	Ser	370	375	380

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Gln	Asp	Ala	Thr	Asp	Tyr	Arg	Leu	Arg	Ser	Leu	Arg	Lys	Leu	Leu	Ala	
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Cys	Asn	Thr	Ser	Gly	Asn	Leu	Leu	Leu	Pro	Glu	Gln	Glu	Ala	Leu	Glu	
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Val	Thr	Arg	Val	Phe	Leu	Lys	Lys	Leu	Asn	Gln	Arg	Ser	Arg	Gly	Arg	
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Tyr	Gln	Leu	Gln	Arg	Ile	Val	Asn	Val	Glu	Lys	Arg	Gln	Asp	Gln	Leu	690	695	700	
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Arg	Val	Val	Arg	Leu	Ser	Glu	Tyr	Val	Ser	Ala	Arg	Gly	Trp	Gln	Gly	725	730	735	
Ile	Asp	Pro	Ala	Gly	Gly	Glu	Glu	Val	Glu	Ala	Arg	Asn	Leu	Gln	Gly	740	745	750	
Leu	Val	Trp	Asp	Pro	His	Asn	Arg	Arg	Arg	Gln	Val	Leu	Asn	Thr	Arg	755	760	765	
Ala	Gln	Glu	Pro	Lys	Leu	Cys	Trp	Pro	Gln	Gly	Phe	Ser	Trp	Ser	His	770	775	780	
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Val	Gln	Gln	Phe	Ile	Lys	Asp	Met	Glu	Asn	Leu	Phe	Gln	Val	Thr	Gly	805	810	815	
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His	Ile	His	Phe	Pro	Ala	Gly	Val	Ile	Asp	Ala	Ile	Arg	Lys	His	Cys	885	890	895	
Val	Glu	Gly	Lys	Met	Ala	Phe	Ala	Pro	Met	Val	Met	Arg	Leu	His	Cys	900	905	910	
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Gly	Leu	Leu	Gly	Ile	Tyr	Lys	Ser	Asp	Leu	Asp	Arg	Ile	Gly	Gly	Met	930	935	940	
Asn	Thr	Lys	Glu	Phe	Arg	Asp	Arg	Trp	Gly	Gly	Glu	Asp	Trp	Glu	Leu	945	950	955	960
Leu	Asp	Arg	Ile	Leu	Gln	Ala	Gly	Leu	Asp	Val	Glu	Arg	Leu	Ser	Leu	965	970	975	
Arg	Asn	Phe	Phe	His	His	Phe	His	Ser	Lys	Arg	Gly	Met	Trp	Ser	Arg	980	985	990	

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 995 998

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 Lys Leu Leu Arg Arg Arg Phe Arg Leu Leu Leu Ala Leu Ala Val Val  
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 Ser Val Gly Leu Trp Thr Leu Tyr Leu Glu Leu Val Ala Ser Ala Gln  
 35 40 45  
 gtc ggc ggg aac ccc ctg aac cgg agg tac ggc agc tgg aga gaa cta 192  
 Val Gly Gly Asn Pro Leu Asn Arg Arg Tyr Gly Ser Trp Arg Glu Leu  
 50 55 60  
 gcc aag gct ctg gcc agc agg aac att cca gct gtg gat cca cac ctc 240  
 Ala Lys Ala Leu Ala Ser Arg Asn Ile Pro Ala Val Asp Pro His Leu  
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 cag ttc tac cat ccc cag agg ctg agc ctc gag gac cac gac att gac 288  
 Gln Phe Tyr His Pro Gln Arg Leu Ser Leu Glu Asp His Asp Ile Asp  
 85 90 95  
 caa ggg gtg agc agt aac agc agc tac ttg aag tgg aac aag cct gtc 336  
 Gln Gly Val Ser Ser Asn Ser Ser Tyr Leu Lys Trp Asn Lys Pro Val  
 100 105 110  
 ccc tgg ctc tca gag ttc cgg ggc cgt gcc aac ctg cat gtg ttt gaa 384  
 Pro Trp Leu Ser Glu Phe Arg Gly Arg Ala Asn Leu His Val Phe Glu  
 115 120 125  
 gac tgg tgt ggc agc tct atc cag cag ctc agg agg aac ctg cat ttc 432  
 Asp Trp Cys Gly Ser Ser Ile Gln Gln Leu Arg Arg Asn Leu His Phe  
 130 135 140  
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 Pro Leu Tyr Pro His Ile Arg Thr Thr Leu Arg Lys Leu Ala Val Ser  
 145 150 155 160  
 ccc aaa tgg acc aac tat ggc ctc cgc atc ttt ggc tac ctg cac ccc 528  
 Pro Lys Trp Thr Asn Tyr Gly Leu Arg Ile Phe Gly Tyr Leu His Pro  
 165 170 175  
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 Phe Thr Asp Gly Lys Ile Gln Phe Ala Ile Ala Ala Asp Asp Asn Ala

180	185	190		
gag ttc tgg ctg agc ctc gat Glu Phe Trp Leu Ser Leu Asp 195	gac cag gtc tca ggc ctc Asp Gln Val Ser Gly Leu Gln 200	cag ctg ctg Leu Leu 205	624	
gcc agt gtg ggc aag act gga aag gag tgg acc gcc ccg gga gag ttt Ala Ser Val Gly Lys Thr Gly Lys Glu Trp Thr Ala Pro Gly Glu Phe 210	215	220	672	
ggg aaa ttt cgg agc caa att tcc aag ccg gtg agc ctg tca gcc tcc Gly Lys Phe Arg Ser Gln Ile Ser Lys Pro Val Ser Leu Ser Ala Ser 225	230	235	240	720
cac agg tac tac ttc gag gtg ctg cac aag cag aat gag gag ggc acc His Arg Tyr Tyr Phe Glu Val Leu His Lys Gln Asn Glu Glu Gly Thr 245	250	255	768	
gac cac gtg gaa gtt gca tgg cga cgg aac gac cct gga gcc aag ttc Asp His Val Glu Val Ala Trp Arg Arg Asn Asp Pro Gly Ala Lys Phe 260	265	270	816	
acc atc att gac tcc ctc tcc ctg tcc ctc ttc aca aat gag acg ttc Thr Ile Ile Asp Ser Leu Ser Leu Ser Leu Phe Thr Asn Glu Thr Phe 275	280	285	864	
cta cag atg gat gag gtg ggc cac atc cca cag aca gca gcc agc cac Leu Gln Met Asp Glu Val Gly His Ile Pro Gln Thr Ala Ala Ser His 290	295	300	912	
gtg gac tcc tcc aac gct ctt ccc agg gat gag cag ccg ccc gct gac Val Asp Ser Ser Asn Ala Leu Pro Arg Asp Glu Gln Pro Pro Ala Asp 305	310	315	320	960
atg ctt cgg cct gac ccc cgg gac acc ctc tat cga gtg cct ctg atc Met Leu Arg Pro Asp Pro Arg Asp Thr Leu Tyr Arg Val Pro Leu Ile 325	330	335	1008	
ccc aag tcg cat ctc cgc cac gtc ctg cct gac tgt ccc tac aaa ccc Pro Lys Ser His Leu Arg His Val Leu Pro Asp Cys Pro Tyr Lys Pro 340	345	350	1056	
agc tat ctg gtg gat ggg ctt cct ctg cag cgc tac cag gga ctc cgg Ser Tyr Leu Val Asp Gly Leu Pro Leu Gln Arg Tyr Gln Gly Leu Arg 355	360	365	1104	
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cac atg gag acc cac aat aaa tgt ttc tac cag gaa aac gcc tac tac His Met Glu Thr His Asn Lys Cys Phe Tyr Gln Glu Asn Ala Tyr Tyr 385	390	395	400	1200
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Lys Gln Gly Leu Glu Gln Pro Gly Phe Glu Glu Asn Leu Leu Glu Glu	
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Asn Ala Arg Met Leu Glu Gly Arg Gln Thr Pro Ala Ser Thr Leu Glu	
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Lys Arg Lys Gln Lys Pro Ser Pro Glu Pro Ser Gln Asp Ser Pro His	
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Val Val Ala Ala Ala Gly Gln Glu Gly Gln Val Glu Gly Glu Glu Glu	
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Gly Glu Glu Glu Glu Glu Glu Glu Asp Met Ser Glu Val Phe Glu Tyr	
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915 920 925	
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Gly Gly Pro Arg Lys Pro Pro Pro Leu Asn Leu Thr His Gln Thr Pro  
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Pro Trp Arg Glu Glu Phe Lys Gly Gln Val Asn Leu His Val Phe Glu  
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Pro Leu Phe Pro His Thr Arg Thr Thr Val Thr Lys Leu Ala Val Ser  
145 150 155 160  
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Ala Arg Asp Gly Asp Ile Gln Phe Ser Val Ala Ser Asp Asp Asn Ser  
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195 200 205  
Ala Phe Val Gly Lys Thr Gly Ser Glu Trp Thr Ala Pro Gly Glu Phe  
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Ile	Gly	Gly	Phe	Pro	Pro	Gln	Gly	Glu	Pro	Ser	Ala	Asp	Met	Leu	His				
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Pro	Arg	Pro	Leu	Pro	Leu	Phe	Leu	Gly	Arg	Ala	Pro	Pro	Pro	Arg	Thr				
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Ser	Tyr	Phe	Asn	Ile	Ile	Leu	Val	Asp	Phe	Glu	Ser	Glu	Asp	Met	Asp



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Lys Arg Thr Gly Asn Phe Glu Arg Ser Ala Gly Leu Gln Thr Gly Val				
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Asp Ala Val Glu Asp Pro Ser Ser Ile Val Phe Leu Cys Asp Leu His				
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Ile His Phe Pro Pro Asn Ile Leu Asp Ser Ile Arg Lys His Cys Val				
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Glu Gly Lys Leu Ala Phe Ala Pro Val Val Met Arg Leu Gly Cys Gly				
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Leu Phe Gly Ile Tyr Lys Ser Asp Phe Asp Arg Val Gly Gly Met Asn				
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Leu Leu Leu Leu Leu Leu Thr Cys Ala Ala Trp Leu Thr Tyr Val His	
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Arg Ser Leu Val Arg Pro Gly Arg Ala Leu Arg Gln Arg Leu Gly Tyr	
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Gly Arg Asp Gly Glu Lys Leu Thr Gly Val Thr Asp Ser Arg Gly Val	
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Arg Val Pro Ser Ser Thr Gln Arg Ser Glu Asp Ser Ser Glu Ser His	
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gaa gag gag cag gcg ccc gag ggg cgg ggc cca aac atg ctg ttt cct	288
Glu Glu Glu Gln Ala Pro Glu Gly Arg Gly Pro Asn Met Leu Phe Pro	
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gga gga cct agg aag cca ccc cca ctg aac ctc acc cac cag aca ccc	336
Gly Gly Pro Arg Lys Pro Pro Pro Leu Asn Leu Thr His Gln Thr Pro	
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Pro Trp Arg Glu Glu Phe Lys Gly Gln Val Asn Leu His Val Phe Glu	
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cca ctc ttt cct cac act cgt act acg gtg aca aag tta gct gtg tcc	480
Pro Leu Phe Pro His Thr Arg Thr Thr Val Thr Lys Leu Ala Val Ser	
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Pro Lys Trp Lys Asn Tyr Gly Leu Arg Ile Phe Gly Phe Ile His Pro	
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Ala Arg Asp Gly Asp Ile Gln Phe Ser Val Ala Ser Asp Asp Asn Ser	
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Glu Phe Trp Leu Ser Leu Asp Glu Ser Pro Ala Ala Ala Gln Leu Val	
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Ala Phe Val Gly Lys Thr Gly Ser Glu Trp Thr Ala Pro Gly Glu Phe	
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Thr Lys Phe Ser Ser Gln Val Ser Lys Pro Arg Arg Leu Met Ala Ser	
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Arg Arg Tyr Tyr Phe Glu Leu Leu His Lys Gln Asp Asp Lys Gly Ser	
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Asp His Val Glu Val Gly Trp Arg Ala Phe Leu Pro Gly Leu Lys Phe	
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gag atc att gat tct gct cac att tcc ctg tac aca gat gag tca tct	864
Glu Ile Ile Asp Ser Ala His Ile Ser Leu Tyr Thr Asp Glu Ser Ser	
275 280 285	

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Gln	Arg	Ala	Ser	Pro	Arg	Ala	Leu	Arg	Asp	Ser	Pro	Trp	Pro	Pro	Phe		
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Pro	Gly	Val	Phe	Leu	Arg	Pro	Lys	Pro	Leu	Pro	Arg	Val	Gln	Leu	Arg		
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Val	Pro	Pro	His	Pro	Pro	Arg	Thr	Gln	Gly	Tyr	Arg	Thr	Ser	Gly	Pro		
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Lys	Val	Thr	Glu	Leu	Lys	Pro	Pro	Val	Arg	Ala	Gln	Thr	Ser	Gln	Gly		
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Asn	Leu	Gln	Leu	Pro	Glu	Ala	Glu	Ala	Val	Asp	Val	Val	Ala	Gln	Tyr		
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ctc ttt ggg atc tac aaa tca gac ttt gac aga gta gga ggc atg aac Leu Phe Gly Ile Tyr Lys Ser Asp Phe Asp Arg Val Gly Gly Met Asn			2928

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Thr Glu Glu Phe Arg Asp Gln Trp Gly Gly Glu Asp Trp Glu Leu Leu				
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Asp Arg Val Leu Gln Ala Gly Leu Glu Val Glu Arg Leu Arg Leu Arg				
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 Gln Val Thr Gly Asp Ala His Phe Ser Ile Ile Ile Thr Asp Tyr Ser  
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 Lys Leu Leu Arg Arg Arg Phe Arg Leu Leu Leu Leu Leu Ala Val Val  
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gcc aag gcc cta gcc agc agg aac atc cca gcc gtt gat ccg aat ctc Ala Lys Ala Leu Ala Ser Arg Asn Ile Pro Ala Val Asp Pro Asn Leu 65 70 75 80			240
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cga agt agg agt agg aac agt agc tac ctg aag tgg aac aag cct gtc Arg Ser Arg Ser Arg Asn Ser Ser Tyr Leu Lys Trp Asn Lys Pro Val 100 105 110			336
ccc tgg ctc tca gag ttc cgg ggc cac gcc aac cta cat gtg ttt gaa Pro Trp Leu Ser Glu Phe Arg Gly His Ala Asn Leu His Val Phe Glu 115 120 125			384
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Phe Val His Leu Ser Phe Val Tyr Pro Asn Asp Tyr Thr Arg Leu Ser	
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His Met Glu Thr His Asn Lys Cys Phe Tyr Gln Glu Ser Ala Tyr Asp	
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Lys His Gly Pro Glu Gln Pro Ala Gly Leu Glu Asp Gly Leu Leu Glu	
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Glu Ser Gln Tyr Glu Asp Val Pro Glu Glu Ile Pro Thr Ser Gln Asp	
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Gln Ser Gly Pro Val Ala Pro Leu Ser Lys Gln Asn Ser Thr Thr Ala	
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